Sonia Fabris

List of Publications by Year in descending order

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Version: 2024-02-01

101384 143772 3,561 92 36 57 citations h-index g-index papers 92 92 92 4994 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Report from the European Myeloma Network on interphase FISH in multiple myeloma and related disorders. Haematologica, 2012, 97, 1272-1277.	1.7	254
2	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. Blood, 2009, 114, e20-e26.	0.6	224
3	A SNP microarray and FISHâ€based procedure to detect allelic imbalances in multiple myeloma: An integrated genomics approach reveals a wide gene dosage effect. Genes Chromosomes and Cancer, 2009, 48, 603-614.	1.5	134
4	Molecular Classification of Multiple Myeloma: A Distinct Transcriptional Profile Characterizes Patients Expressing CCND1 and Negative for 14q32 Translocations. Journal of Clinical Oncology, 2005, 23, 7296-7306.	0.8	123
5	Gene expression profiling of plasma cell dyscrasias reveals molecular patterns associated with distinct IGH translocations in multiple myeloma. Oncogene, 2005, 24, 2461-2473.	2.6	118
6	Cyclin D1 overexpression is a favorable prognostic variable for newly diagnosed multiple myeloma patients treated with high-dose chemotherapy and single or double autologous transplantation. Blood, 2003, 102, 1588-1594.	0.6	113
7	An integrative genomic approach reveals coordinated expression of intronic miR-335, miR-342, and miR-561 with deregulated host genes in multiple myeloma. BMC Medical Genomics, 2008, 1, 37.	0.7	104
8	Differential repetitive DNA methylation in multiple myeloma molecular subgroups. Carcinogenesis, 2009, 30, 1330-1335.	1.3	99
9	Biological and Clinical Relevance of miRNA Expression Signatures in Primary Plasma Cell Leukemia. Clinical Cancer Research, 2013, 19, 3130-3142.	3.2	86
10	Molecular Analysis of 11q13 Breakpoints in Multiple Myeloma. Blood, 1999, 93, 1330-1337.	0.6	80
11	Long non-coding RNA NEAT1 targeting impairs the DNA repair machinery and triggers anti-tumor activity in multiple myeloma. Leukemia, 2020, 34, 234-244.	3.3	80
12	Acquired CYP19A1 amplification is an early specific mechanism of aromatase inhibitor resistance in ERÎ \pm metastatic breast cancer. Nature Genetics, 2017, 49, 444-450.	9.4	77
13	Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia. BMC Medical Genomics, 2013, 6, 27.	0.7	73
14	Immunohistochemical Analysis of Cyclin D1 Shows Deregulated Expression in Multiple Myeloma with the t(11;14). American Journal of Pathology, 2000, 156, 1505-1513.	1.9	72
15	Upregulation of translational machinery and distinct genetic subgroups characterise hyperdiploidy in multiple myeloma. British Journal of Haematology, 2007, 136, 565-573.	1.2	66
16	Molecular spectrum of <i>BRAF, NRAS</i> and <i>KRAS</i> gene mutations in plasma cell dyscrasias: implication for MEK-ERK pathway activation. Oncotarget, 2015, 6, 24205-24217.	0.8	65
17	Molecular characterization of human multiple myeloma cell lines by integrative genomics: Insights into the biology of the disease. Genes Chromosomes and Cancer, 2007, 46, 226-238.	1.5	62
18	Integrative highâ€resolution microarray analysis of human myeloma cell lines reveals deregulated miRNA expression associated with allelic imbalances and gene expression profiles. Genes Chromosomes and Cancer, 2009, 48, 521-531.	1.5	60

#	Article	IF	Citations
19	Genomeâ€wide analysis of primary plasma cell leukemia identifies recurrent imbalances associated with changes in transcriptional profiles. American Journal of Hematology, 2013, 88, 16-23.	2.0	60
20	Clinical Monoclonal B Lymphocytosis versus Rai O Chronic Lymphocytic Leukemia: A Comparison of Cellular, Cytogenetic, Molecular, and Clinical Features. Clinical Cancer Research, 2013, 19, 5890-5900.	3.2	60
21	Analysis of FGFR3 gene mutations in multiple myeloma patients with t(4;14). British Journal of Haematology, 2001, 114, 362-364.	1.2	59
22	Molecular and transcriptional characterization of 17p loss in Bâ€eell chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2008, 47, 781-793.	1.5	59
23	Detection of t(4;14)(p16.3;q32) Chromosomal Translocation in Multiple Myeloma by Double-Color Fluorescent In Situ Hybridization. Blood, 1999, 94, 724-732.	0.6	58
24	Biological and clinical relevance of quantitative global methylation of repetitive DNA sequences in chronic lymphocytic leukemia. Epigenetics, 2011, 6, 188-194.	1.3	58
25	Whole-exome sequencing of primary plasma cell leukemia discloses heterogeneous mutational patterns. Oncotarget, 2015, 6, 17543-17558.	0.8	55
26	Integrative Genomics Analyses Reveal Molecularly Distinct Subgroups of B-Cell Chronic Lymphocytic Leukemia Patients with 13q14 Deletion. Clinical Cancer Research, 2010, 16, 5641-5653.	3.2	52
27	Highâ€throughput sequencing for the identification of <i><scp>NOTCH</scp>1</i> stage chronic lymphocytic leukaemia: biological and clinical implications. British Journal of Haematology, 2014, 165, 629-639.	1.2	52
28	microRNAome Expression in Chronic Lymphocytic Leukemia: Comparison with Normal B-cell Subsets and Correlations with Prognostic and Clinical Parameters. Clinical Cancer Research, 2014, 20, 4141-4153.	3.2	52
29	Definition of progression risk based on combinations of cellular and molecular markers in patients with Binet stage A chronic lymphocytic leukaemia. British Journal of Haematology, 2009, 146, 44-53.	1.2	50
30	Transcriptional Characterization of a Prospective Series of Primary Plasma Cell Leukemia Revealed Signatures Associated with Tumor Progression and Poorer Outcome. Clinical Cancer Research, 2013, 19, 3247-3258.	3.2	50
31	Characterization of oncogene dysregulation in multiple myeloma by combined FISH and DNA microarray analyses. Genes Chromosomes and Cancer, 2005, 42, 117-127.	1.5	49
32	CD26 expression in mature Bâ€cell neoplasia: its possible role as a new prognostic marker in Bâ€CLL. Hematological Oncology, 2009, 27, 140-147.	0.8	46
33	A compendium of <i>DIS3</i> mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget, 2015, 6, 26129-26141.	0.8	40
34	Molecular spectrum of <i>TP53</i> mutations in plasma cell dyscrasias by next generation sequencing: an Italian cohort study and overview of the literature. Oncotarget, 2016, 7, 21353-21361.	0.8	40
35	The transactivating isoforms of p63 are overexpressed in high-grade follicular lymphomas independent of the occurrence ofp63 gene amplification. Journal of Pathology, 2005, 206, 337-345.	2.1	39
36	Relevance of telomere/telomerase system impairment in early stage chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2014, 53, 612-621.	1.5	38

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37	The Role of New Technologies in Myeloproliferative Neoplasms. Frontiers in Oncology, 2019, 9, 321.	1.3	37
38	Relevance of Stereotyped B-Cell Receptors in the Context of the Molecular, Cytogenetic and Clinical Features of Chronic Lymphocytic Leukemia. PLoS ONE, 2011, 6, e24313.	1.1	36
39	Bâ€eell receptor configuration and adverse cytogenetics are associated with autoimmune hemolytic anemia in chronic lymphocytic leukemia. American Journal of Hematology, 2013, 88, 32-36.	2.0	36
40	Integrative genomic analysis reveals distinct transcriptional and genetic features associated with chromosome 13 deletion in multiple myeloma. Haematologica, 2007, 92, 56-65.	1.7	34
41	Compendium of <i><scp>FAM</scp>46C</i> gene mutations in plasma cell dyscrasias. British Journal of Haematology, 2016, 174, 642-645.	1.2	34
42	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-cell Receptors. Clinical Cancer Research, 2012, 18, 1870-1878.	3.2	33
43	Heterogeneous pattern of chromosomal breakpoints involving the MYC locus in multiple myeloma. Genes Chromosomes and Cancer, 2003, 37, 261-269.	1.5	31
44	Circulating tumor DNA as a liquid biopsy in plasma cell dyscrasias. Haematologica, 2018, 103, e245-e248.	1.7	29
45	Chromosome 2p gain in monoclonal Bâ€eell lymphocytosis and in early stage chronic lymphocytic leukemia. American Journal of Hematology, 2013, 88, 24-31.	2.0	27
46	Multiplex ligationâ€dependent probe amplification and fluorescence in situ hybridization to detect chromosomal abnormalities in Chronic lymphocytic leukemia: A comparative study. Genes Chromosomes and Cancer, 2011, 50, 726-734.	1.5	24
47	EGFR through STAT3 modulates ΔN63α expression to sustain tumorâ€initiating cell proliferation in squamous cell carcinomas. Journal of Cellular Physiology, 2013, 228, 871-878.	2.0	24
48	Association between gene and miRNA expression profiles and stereotyped subset #4 B-cell receptor in chronic lymphocytic leukemia. Leukemia and Lymphoma, 2015, 56, 3150-3158.	0.6	23
49	Cyclin D3 Immunoreactivity in Gastrointestinal Stromal Tumors Is Independent of Cyclin D3 Gene Amplification and Is Associated with Nuclear p27 Accumulation. Modern Pathology, 2003, 16, 886-892.	2.9	22
50	IgV gene intraclonal diversification and clonal evolution in B-cell chronic lymphocytic leukaemia. British Journal of Haematology, 2004, 133, 060118040555003.	1.2	20
51	Molecular and transcriptional characterization of the novel $17p11.2\hat{a} \in p12$ amplicon in multiple myeloma. Genes Chromosomes and Cancer, 2007, 46, 1109-1118.	1.5	20
52	Cyclin D3 immunoreactivity in follicular lymphoma is independent of the t(6;14)(p21.1;q32.3) translocation orcyclin D3 gene amplification and is correlated with histologic grade and Ki-67 labeling index. International Journal of Cancer, 2004, 112, 71-77.	2.3	16
53	Repetitive DNA Hypomethylation in Multiple Myeloma. Blood, 2008, 112, 2703-2703.	0.6	16
54	Limits and Applications of Genomic Analysis of Circulating Tumor DNA as a Liquid Biopsy in Asymptomatic Forms of Multiple Myeloma. HemaSphere, 2020, 4, e402.	1.2	15

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55	Triple-Negative Essential Thrombocythemia: Clinical-Pathological and Molecular Features. A Single-Center Cohort Study. Frontiers in Oncology, 2021, 11, 637116.	1.3	15
56	Insulin Growth Factor 1 Receptor Expression Is Associated with NOTCH1 Mutation, Trisomy 12 and Aggressive Clinical Course in Chronic Lymphocytic Leukaemia. PLoS ONE, 2015, 10, e0118801.	1.1	15
57	Prospective validation of a risk score based on biological markers for predicting progression free survival in Binet stage A chronic lymphocytic leukemia patients: Results of the multicenter O LL1â€GISL study. American Journal of Hematology, 2014, 89, 743-750.	2.0	14
58	Deregulation of miRNAs-cMYC circuits is a key event in refractory celiac disease type-2 lymphomagenesis. Clinical Science, 2020, 134, 1151-1166.	1.8	14
59	The clinical and biological features of a series of immunophenotypic variant of Bâ€CLL. European Journal of Haematology, 2010, 85, 120-129.	1.1	13
60	Microenvironmental regulation of the IL-23 R/IL-23 axis overrides chronic lymphocytic leukemia indolence. Science Translational Medicine, 2018, 10 , .	5.8	13
61	Global methylation patterns in primary plasma cell leukemia. Leukemia Research, 2018, 73, 95-102.	0.4	13
62	Time to first treatment and P53 dysfunction in chronic lymphocytic leukaemia: results of the O-CLL1 study in early stage patients. Scientific Reports, 2020, 10, 18427.	1.6	13
63	NEAT1 Long Isoform Is Highly Expressed in Chronic Lymphocytic Leukemia Irrespectively of Cytogenetic Groups or Clinical Outcome. Non-coding RNA, 2020, 6, 11.	1.3	11
64	Molecular and biological characterization of three novel interleukin-6-dependent human myeloma cell lines. Haematologica, 2005, 90, 1541-8.	1.7	11
65	Total body computed tomography scan in the initial workâ€up of Binet stage A chronic lymphocytic leukemia patients: Results of the prospective, multicenter Oâ€CLL1â€GISL study. American Journal of Hematology, 2013, 88, 539-544.	2.0	10
66	Distinct patterns of global promoter methylation in early stage chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2014, 53, 264-273.	1.5	10
67	Intraclonal Cell Expansion and Selection Driven by B Cell Receptor in Chronic Lymphocytic Leukemia. Molecular Medicine, 2011, 17, 834-839.	1.9	9
68	Is ZAP70 still a key prognostic factor in early stage chronic lymphocytic leukaemia? Results of the analysis from a prospective multicentre observational study. British Journal of Haematology, 2015, 168, 455-459.	1.2	9
69	Immunoreactivity for cyclin D3 is frequently detectable in high-grade primary gastric lymphomas in the absence of the $t(6;14)(p21.1;q32.3)$ chromosomal translocation. Journal of Pathology, 2003, 200, 596-601.	2.1	8
70	Relevance of Ras gene mutations in the context of the molecular heterogeneity of multiple myeloma. Hematological Oncology, 2007, 25, 6-10.	0.8	8
71	Clonal reticulohistiocytosis of the skin and bone marrow associated with systemic mastocytosis and acute myeloid leukaemia. Histopathology, 2017, 70, 1000-1008.	1.6	8
72	Anagrelide and Mutational Status in Essential Thrombocythemia. BioDrugs, 2016, 30, 219-223.	2.2	7

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73	Prospective validation of predictive value of abdominal computed tomography scan on time to first treatment in Rai O chronic lymphocytic leukemia patients: results of the multicenter Oâ€ <scp>CLL</scp> 1â€ <scp>GISL</scp> study. European Journal of Haematology, 2016, 96, 36-45.	1.1	7
74	Prognostic Significance of Telomere Length in Chronic Lymphocytic Leukemia Patients in Early Stage Disease,. Blood, 2011, 118, 3890-3890.	0.6	7
75	Clinical, Morphological and Clonal Progression of VEXAS Syndrome in the Context of Myelodysplasia Treated with Azacytidine. Clinical Hematology International, 2022, 4, 52-55.	0.7	7
76	Molecular events underlying interleukinâ€6 independence in a subclone of the CMAâ€03 multiple myeloma cell line. Genes Chromosomes and Cancer, 2014, 53, 154-167.	1.5	6
77	An unusual type of myeloid sarcoma localization following myelofibrosis: A case report and literature review. Leukemia Research Reports, 2017, 8, 7-10.	0.2	6
78	Lymphocyte Doubling Time As A Key Prognostic Factor To Predict Time To First Treatment In Early-Stage Chronic Lymphocytic Leukemia. Frontiers in Oncology, 2021, 11, 684621.	1.3	6
79	Molecular Analysis of 11q13 Breakpoints in Multiple Myeloma. Blood, 1999, 93, 1330-1337.	0.6	6
80	Identification of a novel IGH-MMSET fusion transcript in a human myeloma cell line with the $t(4;14)(p16\hat{A}\cdot 3;q32)$ chromosomal translocation. British Journal of Haematology, 2004, 126, 437-439.	1.2	5
81	Frequency and clinical relevance of coding and noncoding <i>NOTCH1</i> mutations in early stage Binet A chronic lymphocytic leukemia patients. Hematological Oncology, 2020, 38, 406-408.	0.8	5
82	LINC00152 expression in normal and Chronic Lymphocytic Leukemia B cells. Hematological Oncology, 2022, 40, 41-48.	0.8	5
83	Biological and molecular characterization of a rare case of cutaneous Richter syndrome. Hematological Oncology, 2017, 35, 869-874.	0.8	4
84	Clinical categories identified by a new prognostic index reflect biological characteristics of patients in early chronic lymphocytic leukemia: The Gruppo Italiano Studio Linfomi (GISL) experience. Leukemia Research, 2010, 34, e217-e218.	0.4	3
85	Integrating clinical, morphological, and molecular data to assess prognosis in patients with primary myelofibrosis at diagnosis: A practical approach. Hematological Oncology, 2019, 37, 424-433.	0.8	3
86	Impact on thrombotic risk of canonical and atypical CALR mutations in essential thrombocythemia. A single-center cohort study. Thrombosis Research, 2022, 210, 67-69.	0.8	3
87	Primary Soft Tissue Lymphomas: Description of Seven Cases and Review of the Literature. Pathology and Oncology Research, 2017, 23, 281-286.	0.9	2
88	Immunoreactivity for cyclin D1 is a reliable marker of gene aberration in plasma cell myeloma but does not specify patients prognosis. Leukemia Research, 2008, 32, 1628-1632.	0.4	1
89	Demystifying the diagnostic criteria of indolent systemic mastocytosis. Hematological Oncology, 2022, 40, 123-125.	0.8	0
90	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-Cell Receptors. Blood, 2011, 118, 2847-2847.	0.6	0

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#	Article	lF	CITATIONS
91	B-Cell Receptor Configuration and Adverse Cytogenetics Are Associated with Autoimmune Hemolytic Anemia in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 1780-1780.	0.6	O
92	Case Report: Evolution of KIT D816V-Positive Systemic Mastocytosis to Myeloid Neoplasm With PDGFRA Rearrangement Responsive to Imatinib. Frontiers in Oncology, 2021, 11, 734025.	1.3	0